

Q96763US.APP  
SEQUENCE LISTING

<110> HAYASHI, HIROAKI  
INOUE, KENICHIRO  
HOSHINO, MASATERU  
SHIBUYA, MASAOKI  
EBIZUKA, YUTAKA

<120> TRITERPENE HYDROXYLASE

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<140> 10/590,661

<141> 2006-08-25

<150> PCT/JP05/03205

<151> 2005-02-25

<150> JP 2004-049123

<151> 2004-02-25

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<170> PatentIn version 3.3

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<400> 8

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1 5 10 15		
tca acc att ctg ata cgt tcc atc ttc	aag aaa cca cag cgt cta aga	96
Ser Thr Ile Leu Ile Arg Ser Ile Phe	Lys Lys Pro Gln Arg Leu Arg	
20 25 30		
ctc cca ccg ggt cct cca att tca gta	ccc ttg ctg gga cac gcg cca	144
Leu Pro Pro Gly Pro Pro Ile Ser Val	Pro Leu Leu Gly His Ala Pro	
35 40 45		
tat ctc cgt tca ctg ctc cac caa gcc ttg	tac aag cta tca ctg cgc	192
Tyr Leu Arg Ser Leu Leu His Gln Ala	Leu Tyr Lys Leu Ser Leu Arg	
50 55 60		
tat gga ccc ttg atc cac gtc atg atc ggt	tcg aag cac gtg gtg gtg	240
Tyr Gly Pro Leu Ile His Val Met Ile Gly	Ser Lys His Val Val Val	
65 70 75 80		
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Ala Ser Ser Ala Glu Thr Ala Lys Gln	Ile Leu Lys Thr Ser Glu Glu	
85 90 95		
gca ttc tgc aac cgt ccc tta atg ata	gcg agc gag agc cta acc tac	336
Ala Phe Cys Asn Arg Pro Leu Met Ile	Ala Ser Glu Ser Leu Thr Tyr	
100 105 110		
ggc gcg gcg gac tac ttc ttc atc ccc	tac ggc aca tac tgg cgg ttc	384
Gly Ala Ala Asp Tyr Phe Phe Ile Pro	Tyr Gly Thr Tyr Trp Arg Phe	
115 120 125		
ctg aag aag ctc tgc atg acg gag ctt	ctg agc ggg aag acc ctg gag	432
Leu Lys Lys Leu Cys Met Thr Glu Leu	Leu Ser Gly Lys Thr Leu Glu	
130 135 140		
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His Phe Val Arg Ile Arg Glu Ser Glu	Val Glu Ala Phe Leu Lys Arg	
145 150 155 160		
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Met Met Glu Ile Ser Gly Asn Gly Asn	Tyr Glu Val Val Met Arg Lys	
165 170 175		
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Glu Leu Ile Thr His Thr Asn Asn Ile	Ile Thr Arg Met Ile Met Gly	
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Lys Lys Ser Asn Ala Glu Asn Asp Glu	Val Ala Arg Leu Arg Lys Val	
195 200 205		
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Ile Gly Phe Met Arg Pro Leu Asp Leu	Gln Gly Phe Gly Lys Lys Asn	
225 230 235 240		
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Met Glu Thr His His Lys Val Asp Ala	Met Met Glu Lys Val Leu Arg	
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Lys Asp Leu Phe Asp Ile Leu Leu Asn Leu Ile Glu Ala Asp Gly Ala	
275 280 285	
gac aat aag ctc act aga gag agt gcc aaa gcc ttt gct ctg gac atg	912
Asp Asn Lys Leu Thr Arg Glu Ser Ala Lys Ala Phe Ala Leu Asp Met	
290 295 300	
ttc atc gcc ggc aca aac ggc ccc gca agc gtc cta gag tgg tca ctg	960
Phe Ile Ala Gly Thr Asn Gly Pro Ala Ser Val Leu Glu Trp Ser Leu	
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Ala Glu Leu Val Arg Asn Pro His Val Phe Lys Lys Ala Arg Glu Glu	
325 330 335	
att gag tca gtg gta ggc aaa gaa agg ctg gtc aaa gaa tca gac att	1056
Ile Glu Ser Val Val Gly Lys Glu Arg Leu Val Lys Glu Ser Asp Ile	
340 345 350	
ccc aac cta cca tac cta caa gca ttg ctg aag gaa acc cta agg ctg	1104
Pro Asn Leu Pro Tyr Leu Gln Ala Leu Leu Lys Glu Thr Leu Arg Leu	
355 360 365	
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His Pro Pro Thr Pro Ile Phe Ala Arg Glu Ala Met Arg Thr Cys Gln	
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Val Glu Gly Tyr Asp Ile Pro Glu Asn Ser Thr Ile Leu Ile Ser Thr	
385 390 395 400	
tgg gcc att ggt agg gat cca aat tac tgg gat gac gca ctc gag tac	1248
Trp Ala Ile Gly Arg Asp Pro Asn Tyr Trp Asp Asp Ala Leu Glu Tyr	
405 410 415	
aag ccg gag agg ttc ttg ttc tcc gac gac ccg ggc aag agc aag att	1296
Lys Pro Glu Arg Phe Leu Phe Ser Asp Asp Pro Gly Lys Ser Lys Ile	
420 425 430	
gac gtg agg ggg cag tac tat cag ctc ctg ccc ttt ggg agc ggg aga	1344
Asp Val Arg Gly Gln Tyr Tyr Gln Leu Leu Pro Phe Gly Ser Gly Arg	
435 440 445	
aga agc tgc ccc gga gcc tcg cta gcg ttg ctt gtc atg caa gca acg	1392
Arg Ser Cys Pro Gly Ala Ser Leu Ala Leu Leu Val Met Gln Ala Thr	
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Leu Ala Ser Leu Ile Gln Cys Phe Asp Trp Ile Val Asn Asp Gly Lys	
465 470 475 480	
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485 490 495	
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505

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Ala

1542

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Leu Pro Pro Gly Pro Pro Ile Ser Val Pro Leu Leu Gly His Ala Pro  
 35 40 45

Tyr Leu Arg Ser Leu Leu His Gln Ala Leu Tyr Lys Leu Ser Leu Arg  
 50 55 60

Tyr Gly Pro Leu Ile His Val Met Ile Gly Ser Lys His Val Val Val  
 65 70 75 80

Ala Ser Ser Ala Glu Thr Ala Lys Gln Ile Leu Lys Thr Ser Glu Glu  
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Ala Phe Cys Asn Arg Pro Leu Met Ile Ala Ser Glu Ser Leu Thr Tyr  
 100 105 110

Gly Ala Ala Asp Tyr Phe Phe Ile Pro Tyr Gly Thr Tyr Trp Arg Phe  
 115 120 125

Leu Lys Lys Leu Cys Met Thr Glu Leu Leu Ser Gly Lys Thr Leu Glu  
 130 135 140

His Phe Val Arg Ile Arg Glu Ser Glu Val Glu Ala Phe Leu Lys Arg  
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Met Met Glu Ile Ser Gly Asn Gly Asn Tyr Glu Val Val Met Arg Lys  
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Glu Leu Ile Thr His Thr Asn Asn Ile Ile Thr Arg Met Ile Met Gly  
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Lys Lys Ser Asn Ala Glu Asn Asp Glu Val Ala Arg Leu Arg Lys Val  
 195 200 205

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Val Arg Glu Val Gly Glu Leu Leu Gly Ala Phe Asn Leu Gly Asp Val  
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Ile Gly Phe Met Arg Pro Leu Asp Leu Gln Gly Phe Gly Lys Lys Asn  
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Met Glu Thr His His Lys Val Asp Ala Met Met Glu Lys Val Leu Arg  
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Glu His Glu Glu Ala Arg Ala Lys Glu Asp Ala Asp Ser Asp Arg Lys  
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Lys Asp Leu Phe Asp Ile Leu Leu Asn Leu Ile Glu Ala Asp Gly Ala  
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Asp Asn Lys Leu Thr Arg Glu Ser Ala Lys Ala Phe Ala Leu Asp Met  
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305 310 315 320

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325 330 335

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340 345 350

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370 375 380

Val Glu Gly Tyr Asp Ile Pro Glu Asn Ser Thr Ile Leu Ile Ser Thr  
385 390 395 400

Trp Ala Ile Gly Arg Asp Pro Asn Tyr Trp Asp Asp Ala Leu Glu Tyr  
405 410 415

Lys Pro Glu Arg Phe Leu Phe Ser Asp Asp Pro Gly Lys Ser Lys Ile  
420 425 430

Asp Val Arg Gly Gln Tyr Tyr Gln Leu Leu Pro Phe Gly Ser Gly Arg  
435 440 445

Arg Ser Cys Pro Gly Ala Ser Leu Ala Leu Leu Val Met Gln Ala Thr

450

455

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Ser Thr Ile Leu Ile Arg Ser Ile Phe Lys Lys Pro Gln Arg Leu Arg  
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35 40 45  
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Tyr Leu Arg Ser Leu Leu His Gln Ala Leu Tyr Lys Leu Ser Leu Arg  
50 55 60  
tat gga ccc ttg atc cac gtc atg atc ggt tgc aag cac gtg gtg gtg 240  
Tyr Gly Pro Leu Ile His Val Met Ile Gly Ser Lys His Val Val Val  
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Ala Ser Ser Ala Glu Thr Ala Lys Gln Ile Leu Lys Thr Ser Glu Glu  
85 90 95  
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Gly Ala Ala Asp Tyr Phe Phe Ile Pro Tyr Gly Thr Tyr Trp Arg Phe  
115 120 125  
ctg aag aag ctc tgc atg acg gag ctt ctg agc ggg aag acc ctg gag 432  
Leu Lys Lys Leu Cys Met Thr Glu Leu Leu Ser Gly Lys Thr Leu Glu  
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480			
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aat Asn	tac Tyr 170	gag Glu	gtg Val
gtg Val	atg Met	agg Arg 175	aag Lys
528			
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576			
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672			
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720			
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768			
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gct Ala	agg Arg	gct Ala	aag Lys
gaa Glu 265	gat Asp	gct Ala	gac Asp
tct Ser	gat Asp 270	agg Arg	aag Lys
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1104			
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gtg Val	ctg Leu	aag Lys	gaa Glu
acc Thr 365	cta Leu	agg Arg	ctg Leu
1152			
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aga Arg	agc Ser 450	tgc Cys	ccc Pro	gga Gly	gcc Ala	tgc Ser 455	cta Leu	gcg Ala	ttg Leu	ctt Leu	gtc Val 460	atg Met	caa Gln	gca Ala	acg Thr	1392
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gcc Ala	aag Lys	cca Pro	ctc Leu 500	aag Lys	tgc Cys	aag Lys	cct Pro	gtt Val 505	ccg Pro	cgt Arg	ttc Phe	act Thr	ccg Pro 510	ttc Phe	gct Ala	1536
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 35 40 45

Tyr Leu Arg Ser Leu Leu His Gln Ala Leu Tyr Lys Leu Ser Leu Arg  
 50 55 60

Tyr Gly Pro Leu Ile His Val Met Ile Gly Ser Lys His Val Val Val  
 65 70 75 80

Ala Ser Ser Ala Glu Thr Ala Lys Gln Ile Leu Lys Thr Ser Glu Glu

Ala Phe Cys Asn Arg Pro Leu Met Ile Ala Ser Glu Ser Leu Thr Tyr  
100 105 110

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Leu Lys Lys Leu Cys Met Thr Glu Leu Leu Ser Gly Lys Thr Leu Glu  
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195 200 205

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 370 375 380

Val Glu Gly Tyr Asp Ile Pro Glu Asn Ser Thr Ile Leu Ile Ser Thr  
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 405 410 415

Lys Pro Glu Arg Phe Leu Phe Ser Asp Asp Pro Gly Lys Ser Lys Ile  
 420 425 430

Asp Val Arg Gly Gln Tyr Tyr Gln Leu Leu Pro Phe Gly Ser Gly Arg  
 435 440 445

Arg Ser Cys Pro Gly Ala Ser Leu Ala Leu Leu Val Met Gln Ala Thr  
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Leu Ala Ser Leu Ile Gln Cys Phe Asp Trp Ile Val Asn Asp Gly Lys  
 465 470 475 480

Asn His His Val Asp Met Ser Glu Glu Gly Arg Val Thr Val Phe Leu  
 485 490 495

Ala Lys Pro Leu Lys Cys Lys Pro Val Pro Arg Phe Thr Pro Phe Ala  
 500 505 510

Ala